

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/263,689**

DATE: 07/22/1999
TIME: 10:08:40

INPUT SET: S32606.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

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PATENT APPLICATION US/09/263,689**

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47     (i) SEQUENCE CHARACTERISTICS:
48         (A) LENGTH: 1138 base pairs
49         (B) TYPE: nucleic acid
50         (C) STRANDEDNESS: double
51         (D) TOPOLOGY: both
52
53
54     (ii) MOLECULE TYPE: cDNA
55
56
57     (ix) FEATURE:
58         (A) NAME/KEY: CDS
59         (B) LOCATION: 52..1020
60
61
62     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64     TTGGCACGA GAGCTCTTCT CACAGGACCA GCCACTAGCG CACCTCGAGC G ATG GCC      57
65                         Met Ala
66                         1
67
68     TAT GTC CCC GCA CCG GGC TAC CAG CCC ACC TAC AAC CCG ACG CTG CCT      105
69     Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr Leu Pro
70             5           10           15
71
72     TAC TAC CAG CCC ATC CCG GGC GGG CTC AAC GTG GGA ATG TCT GTT TAC      153
73     Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser Val Tyr
74             20          25           30
75
76     ATC CAA GGA GTG GCC AGC GAG CAC ATG AAG CGG TTC TTC GTG AAC TTT      201
77     Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val Asn Phe
78             35          40           45           50
79
80     GTG GTT GGG CAG GAT CCG GGC TCA GAC GTC GCC TTC CAC TTC AAT CCG      249
81     Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe Asn Pro
82             55          60           65
83
84     CGG TTT GAC GGC TGG GAC AAG GTG GTC TTC AAC ACG TTG CAG GGC GGG      297
85     Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln Gly Gly
86             70          75           80
87
88     AAG TGG GGC AGC GAG GAG AGG AAG AGG AGC ATG CCC TTC AAA AAG GGT      345
89     Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys Lys Gly
90             85          90           95
91
92     GCC GCC TTT GAG CTG GTC TTC ATA GTC CTG GCT GAG CAC TAC AAG GTG      393
93     Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr Lys Val
94             100         105           110
95
96     GTG GTA AAT GGA AAT CCC TTC TAT GAG TAC GGG CAC CGG CTT CCC CTA      441
97     Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu Pro Leu
98             115         120           125           130
99

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100	CAG ATG GTC ACC CAC CTG CAA GTG GAT GGG GAT CTG CAA CTT CAA TCA	489		
101	Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu Gln Ser			
102	135	140	145	
103				
104	ATC AAC TTC ATC GGA GGC CAG CCC CTC CGG CCC CAG GGA CCC CCG ATG	537		
105	Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro Pro Met			
106	150	155	160	
107				
108	ATG CCA CCT TAC CCT GGT CCC GGA CAT TGC CAT CAA CAG CTG AAC AGC	585		
109	Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu Asn Ser			
110	165	170	175	
111				
112	CTG CCC ACC ATG GAA GGA CCC CCA ACC TTC AAC CCG CCT GTG CCA TAT	633		
113	Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val Pro Tyr			
114	180	185	190	
115				
116	TTC GGG AGG CTG CAA GGA GGG CTC ACA GCT CGA AGA ACC ATC ATC ATC	681		
117	Phe Gly Arg Leu Gln Gly Leu Thr Ala Arg Arg Thr Ile Ile Ile			
118	195	200	205	210
119				
120	AAG GGC TAT GTG CCT CCC ACA GGC AAG AGC TTT GCT ATC AAC TTC AAG	729		
121	Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn Phe Lys			
122	215	220	225	
123				
124	GTG GGC TCC TCA GGG GAC ATA GCT CTG CAC ATT AAT CCC CGC ATG GGC	777		
125	Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg Met Gly			
126	230	235	240	
127				
128	AAC GGT ACC GTG GTC CGG AAC AGC CTT CTG AAT GGC TCG TGG GGA TCC	825		
129	Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp Gly Ser			
130	245	250	255	
131				
132	GAG GAG AAG AAG ATC ACC CAC AAC CCA TTT GGT CCC GGA CAG TTC TTT	873		
133	Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln Phe Phe			
134	260	265	270	
135				
136	GAT CTG TCC ATT CGC TGT GGC TTG GAT CGC TTC AAG GTT TAC GCC AAT	921		
137	Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr Ala Asn			
138	275	280	285	290
139				
140	GGC CAG CAC CTC TTT GAC TTT GCC CAT CGC CTC TCG GCC TTC CAG AGG	969		
141	Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe Gln Arg			
142	295	300	305	
143				
144	GTG GAC ACA TTG GAA ATC CAG GGT GAT GTC ACC TTG TCC TAT GTC CAG	1017		
145	Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr Val Gln			
146	310	315	320	
147				
148	ATC TAATCTATTC CTGGGGCCAT AACTCATGGG AAAACAGAAT TATCCCCTAG	1070		
149	Ile			
150				
151				
152	GAECTCCTTTC TAAGCCCCTA ATAAAATGTC TGAGGGTGTC TCATGAAAAA AAAAAAAAAA	1130		

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153
154 AAAAAAAA 1138
155
156
157 (2) INFORMATION FOR SEQ ID NO:2:
158
159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 323 amino acids
161 (B) TYPE: amino acid
162 (D) TOPOLOGY: linear
163
164 (ii) MOLECULE TYPE: protein
165
166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
167
168 Met Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr
169 1 5 10 15
170
171 Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser
172 20 25 30
173
174 Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val
175 35 40 45
176
177 Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe
178 50 55 60
179
180 Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln
181 65 70 75 80
182
183 Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys
184 85 90 95
185
186 Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr
187 100 105 110
188
189 Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu
190 115 120 125
191
192 Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu
193 130 135 140
194
195 Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro
196 145 150 155 160
197
198 Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu
199 165 170 175
200
201 Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val
202 180 185 190
203
204 Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile
205 195 200 205

INPUT SET: S32606.raw

206
207 Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn
208 210 215 220
209
210 Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg
211 225 230 235 240
212
213 Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp
214 245 250 255
215
216 Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln
217 260 265 270
218
219 Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr
220 275 280 285
221
222 Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe
223 290 295 300
224
225 Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr
226 305 310 315 320
227
228 Val Gln Ile
229
230
231 (2) INFORMATION FOR SEQ ID NO:3:
232
233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 1545 base pairs
235 (B) TYPE: nucleic acid
236 (C) STRANDEDNESS: double
237 (D) TOPOLOGY: both
238
239 (ii) MOLECULE TYPE: cDNA
240
241
242 (ix) FEATURE:
243 (A) NAME/KEY: CDS
244 (B) LOCATION: 16..948
245
246
247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
248
249 AGAGGCCGGCG GAGAG ATG GCC TTC AGC GGT TCC CAG GCT CCC TAC CTG AGT 51
250 Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser
251 1 5 10
252
253 CCA GCT GTC CCC TTT TCT GGG ACT ATT CAA GGA GGT CTC CAG GAC GGA 99
254 Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly
255 15 20 25
256
257 CTT CAG ATC ACT GTC AAT GGG ACC GTT CTC AGC TCC AGT GGA ACC AGG 147
258 Leu Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/09/263,689**

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Line

Error

Original Text